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Improving adaptation to drought stress in white pea bean (*Phaseolus vulgaris* L): genotypic effects on grain yield, yield components and pod harvest index

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Abstract

Common bean (*Phaseolus vulgaris* L.) is the most important food legume crop in Africa and Latin America where rainfall pattern is unpredictable. The objectives were to identify better yielding common bean lines with good canning quality under drought, and to identify traits that could be used as selection criteria for evaluating drought ~~resistant~~ tolerant genotypes. Thirty-five advanced lines were developed through single seed descent and evaluated with a standard check under drought and irrigated conditions at two locations over two years in Ethiopia. Grain yield (GY), pod number per m^2, seed number per m^2 and seed weight ~~were~~ decreased by 56, 47, 49 and 14 %, respectively under drought stress. Eight genotypes had better yield with good canning quality under drought compared to the check. Moderate to high proportion of genetic effects were observed under drought conditions for GY and yield components compared to genotype x environment effects. Significant positive correlations between GY and pod harvest index (PHI) in drought suggest that PHI could be used as an indirect selection criterion for common bean improvement.

Key words: common bean, drought, grain yield, photosynthate remobilization, genotypic effect.

Introduction

Common bean (*Phaseolus vulgaris* L.) is one of the most important food legume crops for direct human consumption (Beebe 2012). It is mainly grown in Africa and Latin America where seasonal rainfall is inconsistent and soil moisture stress often limits grain yield production (Assefa et al. 2013a, Beebe et al. 2013, Wortmann et al., 1998). Drought stress affects plant growth and development of the crop in these two regions. As much as 60% of the common bean growing area is affected by moderate to severe drought stress each year (Assefa et al. 2013a, Beebe 2012, Rao 2014). In eastern and southern Africa, drought is the major production problem in addition to diseases, and it reduces grain yield by 50 % or more (Wortmann et al. 1998). It is also becoming a major environmental stress contributing to low quality of grain (Beebe 2012). The level of reduction in grain yield is determined by the intensity, type and duration of drought stress (Thung and Rao, 1999, Rao et al. 2016). Therefore, development of drought ~~resistant~~ tolerant common bean cultivars is a strategic approach to reduce yield loss and enhance food and nutritional security in the bean growing regions of Africa and Latin America (~~Rao et al. 2013,~~ Beebe et al. 2013).

Increasing yield under drought conditions has been achieved by plant breeding for numerous crops (Cattivelli et al. 2008). Natural selection favors survival mechanisms under stress whereas plant breeding has emphasized selection for increased economic yield (Blum 2011). Thus breeding for drought ~~resistant~~ tolerant cultivars leads to a better yield advantage as compared to drought sensitive cultivars (Polania et al. 2016~~, Assefa et al. 2013a~~). Notably, drought not only affects the grain yield of the crop but also affects the quality of the seed by reducing seed size, lowering seed weight, extending cooking time and decreasing palatability (Assefa et al. 2013b). In common bean, drought stress impacts yield components, for instance it leads to a lower pod number per plant, seed number per plant and seed weight (Assefa et al. 2013a, Beebe et al. 2013~~, Rao et al. 2013~~). Drought ~~resistance~~ tolerance of common bean is a quantitatively inherited trait controlled by several genes and often affected by environment. The complexity of drought ~~resistance~~ tolerance as a trait has slowed progress in improving grain yield under water limited environment. So understanding physiological and genetic

mechanisms of crop ~~resistance~~ tolerance to drought is important for crop improvement and development of more drought ~~resistant~~ tolerant varieties (Beebe et al., 2013).

Recent advances in crop improvement using physiological mechanisms and advanced plant phenotyping have led to a new vision for improving drought ~~resistance~~tolerance, providing plant breeders with better tools and methods for increasing efficiency in improving grain yield under drought conditions (~~Assefa et al. 2015, Assefa et al. 2013a,~~ Blum 2005~~, Rao 2014~~). Meanwhile, a better understanding of morpho-physiological characteristics of plant growth, biomass partitioning, and grain yield under drought stress also enhances the use of efficient selection criteria for greater response of bean cultivars to drought (Beebe et al. 2013, Rao 2014). Various morpho-physiological mechanisms that account for the ability of plants to adapt to drought are grouped as: drought escape (shortened life cycle), drought avoidance (controlling water loss through the leaf surface), and drought ~~resistance~~ tolerance (withstanding water deficit with low tissue water potential (Levitt 1972)). In common bean, deep rooting ability has also been identified as a major trait that could help improve drought ~~resistance~~tolerance, particularly in deep soils where adapted genotypes with deep and thick rooting systems have the capacity to absorb water from deep soil layers (Beebe et al. 2008, Rao 2001, Rao et al. 2016). Bean cultivars that combine high values of canopy biomass with greater mobilization of photosynthates to grain were identified as drought ~~resistant~~ tolerant cultivars (Rao et al. 2013, Polania et al. 2016). Drought ~~resistant~~ tolerant genotypes that produce greater biomass accumulation under water limited conditions produce more grain yield compared to drought sensitive genotypes (Polania et al. 2016, Assefa et al. 2015).

Pod harvest index (PHI) reflects partitioning of photosynthates to grain under drought conditions (Klaedtke et al. 2012, ~~Assefa et al. 2013a,~~ Polania et al. 2016). Assefa et al. (2013a) reported that improving PHI could be the best way to improve common bean adaptions to drought. Meanwhile, in non-stress environments greater PHI is also a key partitioning index required for improving yield potential of common bean (Polania et al. 2016). Drought causes poor grain quality and low yield if the plant doesn't get enough water during flowering and seed filling stages which is a common scenario that African farmers face. Thus,

developing bean cultivars with greater PHI value could help not only improve adaptation to drought but also contribute to greater grain quality and yield potential. Farooq et al. (2016) reported that drought limits the productivity of grain legumes at all growth stages but its occurrence during reproductive and grain development stages is more drastic and usually results in seed yield loss**.** Condon et al. (2004) also illustrated that partitioning of produced biomass towards the harvested product is a key process in breeding and helps to improve water use efficiency in crop plants.

Although significant progress has been made in improving drought ~~resistance~~ tolerance of different market classes of common bean, improvement of drought ~~resistance~~ tolerance in white pea bean (or navy bean) has lagged; white pea bean is important in Africa, particularly due to its preference in local markets and its good cooking and canning qualities (Assefa et al. 2006, Assefa et al. 2013b). Africa is the biggest producer and major exporter of the small white beans for processing into canned beans, with Ethiopia accounting for about 10% of the global supply (https://ciat.cgiar.org/position-crops/white-gold-beans-to-beat-drought). Like other bean market classes, white pea bean (navy bean) is one of the bean market classes produced in drought affected parts of Africa and is increasingly becoming a commercial commodity for the export market and canning industry given the current trends of urbanization and market globalization (Katungi et al. 2009). The main objectives of this study were to: (i) identify high yielding white pea bean advanced lines with superior canning quality; (ii) estimate genotypic variation in grain yield and other yield related shoot traits; and (iii) identify key shoot traits that could be used as a selection criterion for evaluating white pea bean under drought stress.

Materials and methods

Field locations

Field experiments (drought and irrigated) were conducted over two years' period (2009 and 2010) in the central and southern rift valley regions of Ethiopia. The experiment in Central Rift Valley was conducted at Melkassa Agricultural Research Center (MARC) of the Ethiopian Institute of Agricultural Research, (8° 24' N and 39° 12' E and1550 m above sea level), with average annual rainfall of 750 mm, and maximum and minimum temperature of 28 °C and 14°C, respectively. The soil is sandy loam with a pH of 7. 6. The experimental site in Southern Rift Valley was located at Awassa Agricultural Research Center (AARC) (7°05′ N and 38°29′ E at an elevation of 1750 meter above sea level) with average annual rainfall of 965 mm. The soil at AARC was sandy loam with pH of 7.0.

Comment [TM1]:

Comment [TM2]:

Plant materials

A commercial white pea bean cultivar (Awash-melka) was crossed with SER16 in 2007 at CIAT, Palmira, Colombia, to generate an inbred population through single seed descent breeding method. Awash-melka (PAN 182), a ~~commercial white pea bean~~ variety with good canning quality, and type II growth habit, was released in 1999 in Ethiopia (Legesse et al. 2013). SER16 line from CIAT breeding program, which is a type IIa bush growth habit, has drought ~~resistance~~ tolerance with excellent combining ability. These complementary traits are highly desired in East and Central African bean growing regions. The inbred lines from the crosses were advanced to the F_4 generations and the seeds from each $F_{4:7}$ line were harvested in bulk. The $F_{4:7}$ seeds were shipped to MARC, Ethiopia in 2008. A total of 35 advanced breeding lines (coded as GNL1 to GNL93), and one standard check (Awash-1) were selected and seeds of selected lines were produced at MARC.

Experimental design and sampling procedure

The field trials were conducted under drought and irrigated conditions at MARC (a site used for drought research for East and Central Africa), and AARC (a semi-arid drought prone experimental site) in 2009 and

2010 cropping seasons. The genotypes were hand planted on July 5th and 6th in 2009 for the first season at MARC and AARC, and July 10th and 12th in 2010 for the second season at MARC and AARC, respectively. In each season, the experiment was laid out using a 6 x 6 lattice design with three replications in two-row plots of 3 m in length with a 0.4 m spacing between rows. Two seeds per hole were planted at intra-row spacing of 10 cm. The seedlings were thinned to one plant per hill ten days after emergence. Di-ammonium phosphate (DAP) fertilizer was applied at the rate of 100 kg ha^{-1} as side banding during planting at both sites. Weed control was done manually at both MARC and AARC sites during both 2009 and 2010 experimental seasons.

The genotypes were grown under drought stress (DS) and no stress (NS, control) conditions as described by Beebe et al. (2013). The experimental plots of DS and NS were planted adjacent to each other in the same field separated by a 5m wide buffer zone of a drought ~~resistance~~ tolerance common bean variety (Nasir) to minimize lateral movement of water from irrigated plots to drought plots. Furrow irrigation was applied during experimental period for both DS and NS experiments (approximately 40 mm of water per irrigation) during this period. DS experiment at MARC received a total of three irrigations per year whereas a DS experiment at AARC received a total of two irrigations in each year. In both years, supplemental irrigation was suspended after 80% of flowering was attained at each plot and for the remainder of the crop cycle to induce drought stress (less water availability from flowering to physiological maturity) as demonstrated by Assefa et al. (2013a) and Samson et al. (2006). The NS treatment was irrigated until physiological maturity with a total of six irrigations at MARC and four irrigations at AARC. All genotypes in DS treatment showed wilting symptoms at mid-day during flowering, and drought stress increased throughout pod filling until physiological maturity both at MARC and AARC. Weather data for each growing season was recorded both for MARC and AARC (Table 1).

At the mid-pod filling growth stage, 0.5 m row length from each experimental plot with about 6 plants was used for destructive sampling to measure canopy biomass (CB; leaves + stems + petioles + pods), and dry matter distribution among leaves, stems and pods (Assefa et al. 2013a, Beebe et al. 2013). At maturity, dry weight of stems, pods, pod walls and seeds was determined by harvesting a 0.5 m row length from each plot and

oven dried the same samples at 70 ^{0}C for 48 hrs. One hundred seeds were randomly selected from each plot to determine 100 seed weight (SW). Seeds number per plant and pods number per plant were counted on four randomly selected plants within the sampling area at harvest. Pod harvest index (PHI; dry weight of seed at harvest/ dry weight of pod at harvest), pod number per area (PN; pods m^{-2}), and seed number per area (SN; seeds m^{-2}) was computed as described by Beebe et al. (2013). Days to physiological maturity (DM) was recorded and grain yield (GY) was measured for each experimental plot of kg 2.2 m^{-2} and later GY values were adjusted to 10 % moisture content.

Comment [TM3]:

Canning quality test

Twenty-four better yielding and drought ~~resistant~~ tolerant white pea bean genotypes were selected from MARC during the second year (2010) experimental period. After harvesting, seeds from each genotype were prepared for shipping by hand-cleaning and picking to remove culls and any diseased, discolored or foreign materials present within the collection. These were then sealed in plastic bags and packed in envelop paper before they were shipped from Ethiopia to Italy, where canning quality assessment was carried out by a private sector partner, ACOS, an agricultural commodities supply company in 2010. The samples (500g) included two replicates of each genotype (24 genotypes). Due to the high cost incurred in shipping and determining canning quality, the samples were only taken from MARC drought experiment of the second year's (2010) harvest.

Bean canning process

Bean canning processing was performed at canning bean factory in Molvena, Italy. Two replicates of bean samples (100 g per replicate) for each genotype were tested for cooking quality by measuring time using the automated Matson bean cooker following the method described by Wang et al. (1988). Another two replicates

of beans samples for each genotype was placed for soaking for 30 min at room temperature and then blanched for 30 minutes at 88^{o}C, rinsed in cold flowing water for one minute.

The hydration coefficient (HC) (HC = Mass of soaked beans (g)/ Mass of dry beans (g)) was calculated after soaking, and the washed-drained weight (WDW) (g) was measured after blanching (Van Der Merwe et. Al., 2006). The blanched bean samples were transferred into cans and then 100 g of commercial tomato sauce was added to each can. The cans were sealed with automatic seamer and sterilized. All the cans were stored for two weeks prior to opening for evaluation. After two weeks of storage, the canned beans were reopened and the sauce drained. The visual appearance and physical traits were evaluated using a 1-5 scale. The canning quality measurements included, percent washed drain weight (PWDW) (Washed drained weight (g) / Mass of can contents (g)), clumping (1=very much clumping and 5 = very little clumping), splits (1 = completely broken seed and 5 = seeds without cracks, splits and loose seed coat), shape (1 = elongated seed and 5 = very round seed), and uniformity (1 = very variable and 5 = very uniform seed)

Statistical model and data analyses

~~Statistical model: In this study, w~~We considered eight environments as combinations of years, irrigation treatments, and locations for combined data analysis while we considered four environments as combinations of years, and locations for different irrigation treatments. The following linear mixed model was ~~deployed~~ used in this study:

$$y_{ijk} = \mu + E_i + G_j + GE_{ij} + B_{k(i)} + e_{ijk}$$

Where y_{ijk} is an observation; μ is a population mean; E_i is an environmental effect; G_j is a genotypic (cultivar) effect; GE_{ij} is a genotype-by-environment interaction effect; $B_{k(i)}$ is a block effect within an environment; and e_{ijk} is a random error. We deployed a mixed linear model approach, minimum norm quadratic unbiased estimation (MINQUE) (Rao 1971, Zhu J 1989) to estimate variance components. Genotypic effects as

deviations from the population means for these test lines under two irrigated, non-irrigated, and over two conditions were predicted by adjusted unbiased prediction method (Zhu 1993). A randomized 10-group jackknife method was applied to estimate standard errors for testing significance of all parameters of interest (variance components and genetic effects) (Wu 2012, Wu et al. 2012). Estimation of variance components and prediction of genotypic effects were analyzed by an R package, Minque (Wu 2012). The relationships between drought and irrigated conditions for selected parameters were investigated using Pearson's correlation test (with levels at the probability level of 5% and 1%, respectively). All canning quality trait data and cooking time were statistically analyzed using a complete randomized design of variance in R statistical program. Significant differences among the genotypes were determined at $P < 0.05$ probability level and least significant differences (LSD) were used for mean comparison.

Results

Grain yield (GY) and yield components

Significant genotypic differences were observed in most traits measured including grain yield under drought and irrigated conditions (Fig 1). The mean values for GY (kg/ha) among 36 genotypes ranged from 752 to 1599, and from 2076 to 3355 under drought and irrigated treatments, respectively (Tables 2 and Table 3). The mean values ranged for pod number per area (PN) from 97 to 414, and from 318 to 568; for seed number per area (SN) from 418 to 1463, and from 1304 to 2188; for 100 seed weight (SW) (g) from 17 to 20, and from 20 to 24 under drought and irrigated treatments, respectively. Combined mean values for grain yield (GY) over two years and across two locations ranged from 1544 to 2376 (Table 4). The mean values for GY, PN, SN, and SW under drought condition decreased by 56 %, 47%, 49%, and 14% compared to irrigated conditions, respectively. The eight highest yielding genotypes (GNL43, GNL50, GNL78, GNL60, GNL9, GNL6, GNL22, GNL112) under drought conditions were approximately similar to each other in GY. These genotypes performed better under drought stress with GY ranging from 1397 kg/ha to 1599 kg/ha compared to the standard check (Awash-

1) with an average yield of 1060 kg/ha. Similarly, these genotypes had better mean values for PN, SN and SW under drought conditions compared to the standard check. The lowest ranking genotypes GNL14 and GNL3 had less yield compared to the standard check. All eight drought adapted genotypes were also good performers under irrigated environment (Table 3, Table 4, and Fig 1). Significant disease incidence did not occur during the testing seasons at both experimental sites.

Maturity (DM) and shoot attributes

Significant differences were found among 36 genotypes for days to maturity (DM), canopy biomass (CB) and pod harvest index (PHI) under drought and irrigated conditions (Tables 2, 3, and 4). Drought stress significantly reduced number of days to maturity and CB compared with irrigated experiment. The mean values for DM ranged from 73 to 85 under drought and 92 to 103 under irrigated conditions. The mean values for CB ranged from 2531 kg/ha to 4014 kg/ha under drought conditions and 2853 kg/ha to 4301 kg/ha under irrigated conditions. Mean values for PHI ranged from 65 % to 78 % under drought and from 65 % to 71 % under irrigated conditions (Tables 2 and 3). Seven out of nine top ranking genotypes produced more biomass compared to standard check under the drought conditions. The nine highest ranking genotypes performed better than the standard check for PHI, and they were also significantly different among each other. This top ranking genotypes had 10 % higher in PHI values than the standard check under the drought conditions. The standard check (Awash-1) had the lowest PHI value ~~compared to the rest~~ of all the genotypes studied (Fig. 2).

Variance components

Estimated variance components, expressed as the proportions to the phenotypic variances under drought and irrigated conditions are summarized in Tables 5 and 6. Significant genetic effect variances were detected for all traits under drought and irrigated conditions and were larger than the environmental effects (Table 5 and 6).

Genetic effects variances -were also significant under combined environments (Table 7). Moderate to high genetic effects were observed under drought conditions including 54% for GY, 49% for PN, 46% for SN, 43 % for DM, 75% for CB and 57% for PHI. Genotypic effects played greater role than G x E effects. However, interaction effects had significant role on GY (5%), SN (6%), SW (17%), DM (5%) and PHI (9%). Residual effects contributed to the phenotypic variance values that ranged from 23% to 52 % for the same seven traits that were measured under drought conditions (Table 5)

Significant variance components were also detected for all traits under irrigated conditions except genotype x block interaction (Table 6). A moderate to high genotypic effects were detected for GY (70%), PN (60%), SN (60%), SW (46%), DM (55%), CB (82%) and PHI (27 %), suggesting that the genotypic effects had significant role on these traits. Interestingly, contribution of G x E components for GY was similar under both drought and irrigated conditions. The residual effects contributed to the phenotypic variances ranged from 14 % to 48 % for all seven traits under irrigated conditions. A significant variance component under combined environments (drought and irrigated) was also detected for all traits (Table 7). Environment and G x E interaction effects were more important for GY, SN, SW, CB and PHI under drought conditions than those under irrigated conditions (Table 5 and 6). On the other hand, genotypic effects had greater role only for PHI under drought conditions than irrigated conditions. G x E components under all environments (drought plus irrigated) were significant for all traits ranging from 5% (GY) to 23% (PHI) (Table 7). However, all traits except SW had lower effects compared to drought and irrigated conditions (Tables 5, 6,7).

Predicted genotypic effects and genotypic correlation

The predicted genotypic effects among thirty-six genotypes tested for all the traits under drought, irrigated and combined (drought plus irrigated) conditions are presented in Table 2, 3 and 4 besides the mean data set. Among the 36 genotypes, nine (GNL43, GNL50, GNL78, GNL60, GNL9, GNL6, GNL124, GNL22, GNL112) presented significant desirable positive genotypic effects and had greater mean values than the standard check

(Awash-1) for GY, PN, SN, SW and PHI under drought conditions (Table 2). High yielding genotypes such as GNL43, GNL50, GNL60, GNL9, GNL6, GNL22 and GNL112 had significant positive genotypic effects for CB under drought conditions. Among high yielding genotypes under drought conditions, none of them showed negative genotypic effects for DM. Whereas, the low yielding genotypes such as GNL72, GNL101, GNL79, Awash-1 (standard check), GNL47, GNL52, GNL128, GNL106, GNL3 and GNL14 showed negative genotypic effects (Table2).

Fourteen genotypes (GNL11, GNL76, GNL9, GNL128, GNL50, GNL22, GNL78, GNL43, GNL6, GNL112, GNL60, GNL7, GNL67, GNL14) showed positive genotypic effects for GY under irrigated conditions (Table 3). These genotypes were also better yielding compared to the standard check. Significant positive genotypic effects were detected for PN, SN, SW, and PHI for 11 high yielding genotypes which included GNL11, GNL76, GNL9, GNL128, GNL50, GNL22, GNL78, GNL43, GNL6, GNL112 and GNL60 under irrigated conditions. Among the high yielding genotypes under irrigated condition, eight genotypes GNL76, GNL9, GNL128, GNL50, GNL22, GNL43, GNL6, and GNL60 showed positive genotypic effects for CB under the irrigated conditions.

Eight genotypes (GNL43, GNL50, GNL78, GNL60, GNL9, GNL22, GNL112, GNL6) showed significant positive genotypic effects for GY, PN, SN, SW, and PHI under drought and irrigated conditions. These genotypes also showed positive significant genotypic effects for GY, PN, SN, SW and PHI under combined environments (Table 4). Genetic correlations among seven traits were carried out under drought, irrigated and combined environments (drought plus irrigated conditions) (Table 8 and 9). PN, SN, SW, DM, and PHI had positive and significant genotypic correlation with GY-.

Canning quality and cooking time

Significant differences were found among the tested genotypes for cooking time and canning quality traits. The mean cooking time for all genotypes ranged from 26.1 to 33.9 minutes. Sixteen genotypes had a lower cooking time than the standard check (Awash-1) (Table 10). Hydration coefficient (HC) differed significantly among genotypes and the mean HC of the genotypes ranged from 1.3 to 2.1. Five genotypes including GNL124, GNL6, GNL7, GNL67 and GNL 60 had HC value of 2 and greater. Differences were significant among genotypes for washed-drained weight (WDW) and percent washed-drained weight (PWDW) (Table 10). The genotype GNL78 had the highest WDW (287.5) and GNL35 had the lowest. For PWDW, GNL78 (70 %) had the highest and GNL85 the lowest (58.7 %).

The uniformity (1-5) ranged from 3 to 4.4, and here 11 genotypes had uniformity values greater than or equal to 4 whereas GNL6 had the lowest uniformity. Eight genotypes had the split value greater than or equal to 4 whereas five genotypes had split values less than 3 (Table 10). Degree of clumping and seed size were also evaluated during the canning quality test.

Discussion

Grain yield and yield components

Comment [TM4]:

Results from this study showed the potential of continued adaptation of white pea bean to semi-arid bean growing environments of the central and lower rift valley of Ethiopia, where drought is one of the major bean production problems. MARC was warmer and had more evapotranspiration and less rainfall than AARC. These weather conditions at MARC resulted in more drought stress than at AARC. Significant differences were observed among tested genotypes for GY, yield components, and shoot attributes under drought and irrigated conditions, indicating that there is ample genetic variability among the genotypes for improving ~~resistance~~

tolerance to drought stress. GY and yield components were significantly decreased under drought conditions in both locations and years, indicating that the testing environments were conducive and effective for the purpose of our study. Meanwhile G x E components under both environments (drought ~~plus~~ as well as irrigated) were significant for all traits ranging from 5% (GY) to 23% (PHI) (Table 7). This suggests that the genetic expression of these traits was influenced by the environments.

Grain yield (GY) is the most dependable measurement of drought ~~resistance~~ tolerance in common bean (Assefa et al. 2015, Rao et al. 2013, Ramirez-Vallejo and Kelly 1998). Drought stress can cause yield reduction ranging from 22 to 71 % in common bean (Ramirez-Vallejo and Kelly 1998). Similarly, GY under rain-fed conditions was shown to be reduced by 31 % when compared with fields under irrigation conditions (Rao et al. 2013). Drought also reduced pod number per area (PN) by 63.3 %, seed number per area (SN) by 28.9 % and 100 seed weight (SW) by 22.3 % (Nuñez et Barrios et al. 2005). PN reduction during pod formation is a critical stage in common bean that could cause yield reduction by 40% (Castañeda-Saucedo et al. 2009). In this study, eight genotypes (GNL 43, GNL50, GNL78, GNL60, GNL9, GNL6, GNL112, GNL22) had favorable genotypic values for GY, PN, and SN in drought and irrigated conditions (Fig. 1). On the other hand, poor performing genotypes including the standard check (GNL14, GNL3, GNL106, GNL128, GNL52, GNL47, Awash-1) showed slow pod filling and weak development of pods (PN) under drought conditions. This caused a smaller number of seeds per area (SN) as moisture stress extended from pod formation to maturity, suggesting that PN, followed by SN were important yield related traits that were significantly affected by moisture stress (~~Assefa et al. 2015,~~ Assefa et al. 2013a, Rao et al. 2013). Szilagyi (2003) reprted that PN is a main yield component that caused significant seed yield reduction under drought conditions. Conversely, the same traits (PN and SN) were found to be important for greater seed yield in common bean under non-stress environments (Szilagyi 2003). Similarly, Beebe et al. (2008) reported that improved sink strength caused yield advantage of selected F6:8 genotypes over the check cultivar 'Tio Canela' under terminal drought stress conditions. In our study, values for SN were greater for drought adapted lines than for drought sensitive lines and the check genotype under DS

conditions. This implies that drought ~~resistant~~ tolerant lines have better sink strength as shown by their ability to better remobilize photosynthates into pods and from pods to the seeds (~~Assefa et al. 2013b,~~ Rao et al. 2009, 2013). Significant positive genotypic correlation was found between GY and other plant traits (PN, SN, SW, DM and PHI) under drought and irrigated conditions, validating previous reports (Polania et al. 2016, ~~Assefa et al. 2015,~~ Assefa et al. 2013a, Klaedtke et al. 2012). This indicated that drought ~~resistant~~ tolerant genotypes also responded to irrigated conditions. In this study, selection for greater seed yield under drought also allowed the identification of lines with superior performance under irrigation (Polania et al. 2016, ~~Assefa et al. 2015,~~ Assefa et al. 2013a).

Seed weight (SW) was reduced by 14% under drought conditions compared to irrigated conditions, corroborating the previous findings made by Assefa et al. (2013a, 2015) ~~, Assefa et al. (2013a),~~ and Muñoz-Perea et al. (2006). We observed that drought ~~resistant~~ tolerant lines in this study had relatively bigger seed sizes (SW values greater than 18 g) compared to the standard check (Awash-1). This might be due to better seed filling that improved seed size and also improved seed quality (Assefa et al. 2015, Beebe et al. 2008). Besides contributing to GY, greater SW values could also be an advantage since bigger sized seeds have better canning quality and cooking time than the small sized seeds. This shows that drought ~~resistant~~ tolerant lines with higher SW values have better commercial value for both domestic and international market requirements.

Maturity (DM) and shoot attributes

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In this study, days to maturity (DM) values were lower under drought than irrigated conditions as might be expected. The bean lines under drought conditions matured physiologically ~~at~~ 15 days earlier than the genotypes under irrigated conditions, suggesting that drought ~~resistant~~ tolerant genotypes are able to complete their life cycles earlier during the growing season before soil and crop water deficits occur (Beebe et al. 2013). Notably, drought ~~resistant~~ tolerant genotypes are not only early to flower but also early to mature depending on the level of drought stress (Beebe et al. 2013). This observation is consistent with several previous reports (Assefa et al.

2015, Ramirez-Vallejo and Kelly, 1998, Terán and Singh 2002b, Terán and Singh 2002a). Rainfall distribution and rainfall amount are the major factors for common bean production and therefore matching the phenological development such as flowering time and physiological maturity to the environmental factors and rainfall pattern is considered as an essential criterion for improving drought ~~resistance~~ tolerance in common bean lines (Assefa et al. 2015, ~~Beebe et al. 2013,~~ Beebe et al. 2008, 2011, Ludlow and Muchow 1990).

Drought stress significantly reduces canopy biomass (CB) in common bean (Polania et al. 2016, ~~, Assefa et al. 2015, Assefa et al. 2013a,~~ Rao et al. 2013). In this study, significant CB reduction of all lines was observed under drought conditions, showing that drought has significant impact on CB. However, wide genetic variability was observed among lines in terms of accumulation of CB during drought stress, indicating a better opportunity for selection under drought conditions for this trait rather than under irrigated conditions. Six genotypes (GNL43, GNL50, GNL60, GNL9, GNL6, GNL124) had relatively higher CB values among several better yielding lines under drought stress. This suggests that these lines have better remobilization of photosynthate to pods and from pod walls to seeds (Polania et al. 2016~~, Assefa et al. 2015~~). Specht et al.(2001) reported that plants changing in partitioning of photosynthate to reproductive parts during early growth stage is considered as an adaptive response to drought stress of ~~resistant~~ tolerant lines.

Efficient remobilization of photosynthate or greater partitioning of dry matter to grain yield has been emphasized as an important drought ~~resistance~~ tolerance mechanism in common bean (Assefa et al. 2015, Beebe et al. 2013, Klaedtke et al. 2012). Recently, Polania et al. (2016) and Assefa et al. (2013a) reported that higher values of pod harvest index (PHI) reflect the extent of remobilization of photosynthates from vegetative parts of the plant to pod walls and from pod walls to the seeds. ~~In this study, w~~We observed a strong and significant correlation between GY and PHI under both drought and irrigated conditions but, drought ~~resistant~~ tolerant genotypes had greater photosynthate partitioned from pod wall to developing grain. This emphasizes the importance of photosynthates remobilization for grain filling (Polania et al. 2016, Assefa et al. 2013a). Assefa et al. (2013a) recommended that maintaining a high PHI value can be used as a good strategy for

improving common bean yield under drought conditions. These authors also emphasized that PHI could be an important physiological trait for improving dry matter partitioning to grain for genotypes selected under drought stress and can also be crucial for varietal development and thus has significance for practical bean breeding. Positive correlations of PHI with GY, PN, SN, and SW under drought stress indicates that the lines tested under drought had higher GY mainly due to remobilization of a greater proportion of photosynthate from pods to seeds. The genetic effect observed for the PHI (Table 2) highlighted that genetic factors could play significant role for this trait. This suggests that increased selection pressure for PHI could help to identify promising drought ~~resistant~~ tolerant lines (Assefa et al. 2013a). Similarly, Polania et al. (2016) and Klaedtke et al. (2012) also reported strong relationships between PHI and other shoot traits for genotypes tested under drought, emphasizing that increased photosynthate mobilization from pod wall to seed formation would be an important plant attribute to screen when breeding for drought ~~resistance~~tolerance. In our study, PHI had significant positive correlation with GY under irrigated conditions, indicating that photosynthate remobilization is also crucial in improving yield potential under irrigated conditions (Polania et al. 2016, Assefa et al. 2013a, Klaedtke et al. 2012). In this study, three genotypes including GNL5, GNL85 and GNL 94 were superior in remobilizing photosynthate from vegetative parts to pod formation, but they had moderate levels of grain yield compared to better yielding genotypes under drought. This implies that yield was limited in the final step by poor remobilization of photosynthates to seeds from the pod walls. ~~Similarly,~~ Beebe et al. (2009) reported that significant differences were observed among common bean genotypes for photosynthate remobilization from pod walls to seeds, and described this phenomenon as “lazy pod syndrome” since these genotypes fail to fulfil this very last, and critical step of seed yield production. This was confirmed by other ~~researchers~~ investigators (Polania et al. 2016, Beebe et al. 2013, Klaedtke et al. 2012). Thus we suggest PHI as a physiological trait that is relatively easy to measure and appears to be a very important yield determining factor under different environmental conditions.

Canning quality and cooking time

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In our study, the common bean genotypes evaluated under drought had cooking time ranging from 26.1 to 33.9 minutes. A similar result is reported for cooking time difference among genotypes by Mekonnen and Admassu (2012) and Assefa et al. (2013b). Fast cooking genotypes are needed by local consumers and bean processers and in turn this will reduce cooking time and energy costs. Cooking time is therefore a crucial bean quality trait that significantly influences the consumers' choices. In the current study sixteen genotypes had lower cooking time with superior yield and other traits compared to~~with~~ the standard check. Thus these genotypes can be recommended for release as new fast cooking varieties. Hydration coefficient is one of canning bean traits crucial for canning bean factory. Ghaderi et al. (1984) reported that lower HC values requires more quantities of beans to fill a given can volume, suggesting that higher values of HC are correlated with good canning yield. The HC values of five genotypes (GNL6, GNL124, GNL7, GNL67, GNL 60) are comparable with HC reported by Mekonnen and Admassu (2012). Similarly, the results from this study were consistent with findings reported by Warsame and Kimani (2014). In general, genotypes with better yield potential and good seed size under drought could have potential for better HC. In this study, a significant number of genotypes had PWDW greater than 60%, suggesting that these genotypes met the required criterion of 60% PWDW desired ~~for~~ by bean processors (Balasubramanian et al. 1999). Generally, ~~in this study,~~ a significant number of genotypes were identified for canning quality, suggesting that these genotypes met international canning quality standards, plus local preferences.

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Conclusions

Thirty-six genotypes were evaluated in two cropping seasons and at two locations, and we identified eight genotypes (GNL43, GNL50, GNL78, GNL60, GNL9, GNL6, GNL22, GNL112) that were better adapted to drought conditions. The increase in grain yield of these genotypes was associated with several shoot traits including PN, SN, SW, DM, CB and PHI under drought conditions. In addition, these genotypes also showed good canning quality traits and lower cooking time compared to the standard check, and these improved canning quality traits are demanded by bean processers. This demonstrates that these high yielding genotypes

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can be used as drought ~~resistant~~ tolerant parents in white pea bean cultivar development program. Moderate to high proportion of genetic effects were observed under drought conditions for GY, PN, SN, DM, CB and PHI compared to G x E interaction effects, suggesting that genotypic effects played a greater role than G x E effects. A significant correlation was found between GY, yield components and shoot attributes under drought conditions over two years and two locations. We suggest that PHI is a key shoot trait that is relatively easy to measure and appear to be an important yield determining factor under drought, and should therefore be considered as an indirect selection criterion when breeding for drought tolerance in any white pea bean breeding program.

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Conflict of Interest

All the authors declare that they have no conflict of interest

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Tables

Table 1. Weather conditions during crop growing season at Melkassa and Awassa, Ethiopia (June to October, 2009 & 2010)

Table 2, Phenotypic mean values (PM) and predicted genotypic effects (G) of 36 genotypes for yield, yield related components and shoot traits evaluated under drought conditions at MARC and AARC in 2009 and 2010

Table 3, Phenotypic mean values (PM) and predicted genotypic effects (G) of 36 genotypes for yield, yield related components and shoot traits evaluated under irrigated conditions at MARC and AARC in 2009 and 2010

Table 4, Phenotypic mean values (PM) and predicted genotypic effects (G) of 36 genotypes for yield, yield related components and shoot traits evaluated under combined environments at MARC and AARC in 2009 and 2010

Table 5. Estimated variance components expressed as proportions to the phenotypic variances for all traits under drought environments

Table 6. Estimated variance components expressed as proportions to the phenotypic variances for all traits under irrigated conditions

Table 7. Estimated variance components expressed as proportions to the phenotypic variances for all traits under all environments

Table 8. Genotypic correlation analysis under drought (a) and irrigated (b) environments

Table 9. Genotypic correlation analysis under all environments

Table 10. Canning quality traits of white pea bean genotypes

Figures

Fig. 1: Average grain yield (kg/ha) of genotypes under drought and irrigated conditions at Melkassa and Awassa, Ethiopi**a**. Mean values for two seasons (2009, 2010) and two locations were used. Better yielding genotypes both under drought and irrigated conditions indicated in upper, right hand quadrant

Fig. 2: Relation between grain yield (kg/ha) and pod harvest index (PHI) under drought stress at Melkassa and Awassa**,** Ethiopia. Mean values for two seasons (2009, 2010) and two locations were used. Genotypes with better grain yield and pod harvest index (PHI) indicated in the upper, right hand quadrant

Table 1. Weather conditions during crop growing season at Melkassa and Awassa, Ethiopia (June to October, 2009 & 2010)

	Melkassa 2009						Awassa 2009					
	Rainfall	Temperature (^{0}C)		RH	SH	Evap	Rainfall	Temperature (^{0}C)		RH	SH	Evap
	(mm)	Max	Min	(%)	(hr^{-1} day)	(mm)	(mm)	Max	Min	(%)	(hr^{-1} day)	(mm)
June	25.8	27.9	10.2	51	8	172	60	26.3	11.3	69.1	8.2	166
July	50.2	26.5	11.3	56	7.2	157	64.2	27	11.4	69	7.3	165
August	40.4	25.9	11.8	63	7.2	118.6	109	24.2	12.2	66	7.1	155
September	38	27.7	10.4	57	8.3	123.4	87	26.4	12.1	54	8.1	135
October	15	28.2	9.9	47	8.8	120.3	59	28.9	11.3	48	8.2	121
Mean	169.4[a]	27.2	10.7	54.8	7.9	138.3	379.2	26.56	11.66	61	7.8	148
	Melkassa 2010						Awassa 2010					
	Rainfall	Temperature (^{0}C)		RH	SH	Evap	Rainfall	Temperature (^{0}C)		RH	SH	Evap
	(mm)	Max	Min	(%)	(hr^{-1} day)	(mm)	(mm)	Max	Min	(%)	(hr^{-1} day)	(mm)
June	21	29.4	11.1	52	8.5	185	32	28	13	70	8.3	180
July	41	26.2	11.6	60	7.5	160	100	28	13	71	6.3	165
August	32	25.9	11.3	68	7.8	134	67	26	13.3	69	6.3	140
September	42	27.2	10.8	59	8.6	140	62	26.6	12.7	69	7.3	138
October	12	28.5	9.5	42	8.9	164	26	27.8	11.9	46	9.9	184
Mean	128[a]	27.4	10.9	56.2	8.3	156.6	287	27.28	12.78	65	7.6	161

[a] Total rainfall during the growing season. RH= Relative humidity, SH= Sunshine hour in day, Evap= Evaporation.

Source: Melkassa Agricultural Research Meteorology Station and Awassa Agricultural Research Meteorology Station.

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Table 2, Phenotypic mean values (PM) and predicted genotypic effects (G) of 36 genotypes for yield, yield related components and shoot traits evaluated under drought conditions at MARC and AARC in 2009 and 2010

Lines	GY		PN		SN		SW		DM		CB		PHI	
	PM	G	PM	G	PM	G	PM	G	PM	G	PM	G	PM	G
GNL43	1599	429**	401	169**	1417	523**	20	1.03**	85	4.27**	3362	173**	0.76	0.06**
GNL50	1572	403**	382	151**	1426	534**	20	0.81**	84	3.96**	3668	477**	0.74	0.04**
GNL78	1560	389**	414	183**	1463	569**	19	0.17**	85	4.4**	2944	-244**	0.75	0.05**
GNL60	1514	345**	371	141**	1377	485**	19	0.31**	84	4.01**	3514	324**	0.7	
GNL9	1504	335**	383	152**	1381	490**	19	0.33**	84	3.63**	3427	238**	0.78	0.08**
GNL6	1468	300**	349	120**	1364	475**	20	1.07**	84	4.04**	3742	551**	0.7	
GNL124	1428	261**	321	92**	1173	292**	19	0.59**	83	2.75**	3022	-165**	0.74	0.04**
GNL22	1415	250**	335	105**	1265	377**	19	0.47**	84	3.23**	3650	457**	0.76	0.06**
GNL112	1397	230**	345	115**	1120	239**	19	0.45**	83	2.91**	3310	120**	0.74	0.04**
GNL11	1186	27**	209	-17*	822	-49	19	0.13	82	1.48**	2830	-355**	0.69	-0.01
GNL18	1177	20**	216	-9	824	-43	18	-0.18	82	1.16*	2948	-238**	0.7	0.01
GNL27	1166	9	236	10	918	45	17	-0.77**	81	0.52	3002	-185**	0.68	-0.02*
GNL5	1163	5	186	-39**	782	-85	19	0.68*	82	1.54**	4014	819**	0.68	-0.02**
GNL90	1150	-8	218	-8	833	-38	18	-0.31*	81	0.33	3292	104**	0.71	0.01
GNL48	1148	-9	185	-40**	753	-112**	18	-0.33**	81	0.67*	3155	-29	0.69	-0.01
GNL35	1144	-14	193	-32**	766	-101**	18	-0.5**	81	0.67**	2664	-521**	0.7	0.03**
GNL94	1137	-19	217	-8	797	-74	19	0.43*	80	0.12	3462	266**	0.73	0.03**
GNL76	1125	-33	239	12	924	51	17	-0.78**	80	0.2	2567	-619	0.69	-0.01*
GNL1	1117	-40**	148	-75**	681	-185**	19	0.36**	81	0.43**	2765	-420**	0.7	0.02
GNL85	1084	-72**	168	-56**	694	-171**	19	0.11	80	-0.12	3211	23	0.67	-0.03**
GNL67	1081	-75**	211	-15	785	-81	18	-0.44*	80	-0.2	3902	708**	0.68	-0.02
GNL7	1080	-75*	219	-7	859	-13	17	-0.78**	79	-0.88	3543	352**	0.68	-0.02
GNL93	1078	-78**	186	-39**	744	-123**	18	-0.53*	80	-0.13	3055	-130*	0.68	-0.02
GNL56	1067	-88**	193	-32**	799	-70**	18	-0.56*	79	-1.07*	3531	342**	0.69	-0.01
GNL114	1060	-95*	218	-8	831	-38	18	0.02	79	-1.4*	2951	-236**	0.69	-0.01
GNL10	1060	-94**	187	-38**	763	-104**	19	0.11	80	0.11	2992	-195**	0.68	-0.02**
GNL72	1057	-98**	159	-65**	657	-206**	19	0.41*	79	-1.44**	2871	-314**	0.68	-0.02**
GNL101	1042	-113**	190	-35	738	-128	19	0.27	79	-1.15*	3093	-94*	0.68	-0.02**
GNL79	1011	-143**	160	-63**	682	-184**	18	-0.09	78	-2.24**	2799	-387**	0.68	-0.02**
Awash-1	990	-163**	132	-91**	566	-294**	18	-0.49**	79	-1.33**	2992	-196**	0.65	-0.05**
GNL47	909	-242**	164	-59**	650	-215**	17	-0.81**	76	-4.06**	2531	-653**	0.68	-0.02**
GNL52	900	-251**	106	-116**	464	-390**	18	0.06	76	-4.62**	2622	-562**	0.66	-0.04**

Comment [TM2]: 2nd Reviewer comments

Comment [TM3]: 2nd Reviewer comments

GNL128	871	-278**	132	-90**	558	-300**	18	-0.11	75	-5.33**	2575	-609**	0.66	-0.04**
GNL106	864	-285**	128	-94**	569	-291**	18	-0.55**	76	-4.19**	4012	820**	0.66	-0.03**
GNL3	809	-338**	97	-125**	418	-435**	19	0.1**	75	-5.31**	3061	-125**	0.66	-0.04**
GNL14	752	-393**	132	-91**	505	-352**	17	-0.7**	73	-6.94**	3693	499**	0.65	-0.05**
Mean	1158		226		871		18		80		3188		0.7	
LSD(0.05)	129		62		201		1		2		186		0.0	

*, ** **indicates** significant at 0.05 and 0.01 probability level, respectively. *LSD* least significant difference, *GY* grain yield (kg/ha), *PN* pod number per area (PN: pods m^{-2}), *SN* seed number per area (SN: seeds m^{-2}), *SW* 100 seed weight (g), *DM* days to maturity, *CB* canopy biomass (kg/ha), *PHI* pod harvest index (%)

Comment [TM4]: Reviewer 2

Comment [TM5]:

Comment [TM6]: Reviewer 2

Table 3, Phenotypic mean values (PM) and predicted genotypic effects (G) of 36 genotypes for yield, yield related components and shoot traits evaluated under irrigated conditions at MARC and AARC in 2009 and 2010

Lines	GY		PN		SN		SW		DM		CB		PHI	
	PM	G	PM	G	PM	G	PM	G	PM	G	PM	G	PM	G
GNL11	3355	674**	568	135**	2181	434**	24	2.02**	103	6.14**	3519	-181**	0.71	0.03**
GNL76	3318	637**	560	128**	2188	441**	23	1.54**	102	5.45**	3500	200**	0.69	0.02**
GNL9	3249	569**	541	109**	2173	426**	23	1.82**	98	1.87**	3886	183**	0.71	0.02**
GNL128	3118	439**	533	102**	2092	345**	23	1.08**	101	4.97**	3811	108**	0.7	0.03**
GNL50	3078	402**	494	64**	2007	266**	23	1.03**	98	1.95**	3857	153**	0.7	0.04**
GNL22	3073	398**	523	93**	2118	373**	23	1.72**	100	3.56**	4023	318**	0.71	0.02**
GNL78	3052	377**	479	51**	1935	197**	23	1.34**	100	3.14**	3409	-291**	0.7	0.03**
GNL43	3045	372**	497	68**	1994	254**	23	1.28**	98	1.56**	3774	72**	0.71	0.02**
GNL6	3041	365**	525	94**	2150	401**	23	1.18**	98	1.39**	4256	548**	0.71	0.02**
GNL112	3015	341**	511	82**	1995	253**	22	0.95**	99	2.83**	3736	32	0.69	0.02
GNL60	2995	322**	500	70**	2011	270**	22	0.81**	99	2.48**	3959	254**	0.7	0.02**
GNL7	2947	275**	509	79**	2076	332**	22	0.18	100	3.9**	4123	418**	0.71	0.03**
GNL67	2887	221**	474	45**	1815	80	23	1.13**	101	4.57**	4050	346**	0.69	0.01
GNL101	2873	203**	416	-10	1610	-116**	22	0.99**	98	1.96	3487	-215	0.68	0.01
GNL14	2801	132*	421	-5	1911	174**	21	-0.29	97	0.77	4130	423**	0.68	0.02
GNL94	2740	72	435	8	1662	-67	22	0.79**	97	0.43	3746	43**	0.71	0.02**
GNL10	2711	45*	421	-6	1646	-83**	21	-0.24*	97	0.85**	3411	-289**	0.68	0.02
GNL35	2633	-32	382	-43**	1732	-0.61	21	-0.56*	96	-0.63	3566	-134**	0.66	-0.02**
Awash-1	2588	-75**	395	-30**	1562	-164**	21	-0.26	97	0.53	3268	-429**	0.67	-0.01
GNL18	2570	-95	387	-38*	1668	-62	20	-0.87**	95	-1.35	3491	-210**	0.67	-0.01
GNL72	2546	-116**	380	-44**	1541	-184**	21	-0.74**	95	-0.91	3459	-240**	0.66	-0.02**
GNL114	2435	-223**	404	-22**	1601	-126**	20	-0.85**	93	-3.06	3766	63**	0.67	-0.01**
GNL48	2423	-236**	374	-50**	1531	-194**	20	-1.1**	95	-1.54**	3563	-138		
GNL106	2391	-266**	395	-31**	1602	-123**	21	-0.5**	93	-2.91**	4190	481**	0.67	-0.01*
GNL27	2362	-297**	360	-64**	1547	-179**	20	-1.47**	93	-3.07**	3491	-210**	0.68	0.01
GNL56	2332	-325**	354	-69**	1428	-293**	21	-0.73**	94	-2.13	3812	109**	0.67	-0.01
GNL85	2327	-331**	359	-65**	1324	-391**	20	-0.98**	94	-2.18**	3429	-271**	0.65	-0.03**
GNL47	2319	-337**	345	-78**	1440	-280**	20	-1.13**	93	-2.88**	2853	-841**	0.67	-0.01
GNL3	2315	-341**	371	-53**	1620	-107**	21	-0.69**	94	-2.02**	3528	-172**	0.66	-0.02
GNL124	2277	-380**	364	-61**	1502	-222**	20	-1.08**	92	-3.88**	3710	7	0.68	0.01
GNL1	2275	-380**	369	-55**	1536	-188**	21	-0.67**	93	-2.74**	4009	305**	0.68	-0.01
GNL79	2246	-404**	353	-71**	1434	-288**	20	-1.08**	92	-4.5**	4003	299**	0.68	-0.01
GNL5	2223	-432**	344	-79**	1570	-148**	20	-1.08**	93	-3.2**	4301	593**	0.66	-0.02**
GNL52	2187	-467**	362	-63**	1462	-260**	20	-1.38**	92	-3.92**	2956	-736**	0.66	-0.02**
GNL90	2121	-532**	335	-87**	1359	-359**	20	-1.09**	93	-3.29**	3668	-34**	0.67	-0.01
GNL93	2076	-575**	318	-104**	1304	-413**	20	-1.05**	92	-4.14**	3537	-164**	0.67	-0.01

Comment [TM7]: 2nd Reviewer comments

Mean	2665	427	1731	21	96	3702
LSD(0.05)	136	36	132	0.6	2	107

*, ** **indicates** significant at 0.05 and 0.01 probability level, respectively,. *LSD* least significant difference, *GY* grain yield (kg/ha), *PN* pod number per area (PN: pods m^{-2}), *SN* seed number per area (SN: seeds m^{-2}), *SW* 100 seed weight (g), *DM* days to maturity, *CB* canopy biomass (kg/ha), *PHI* pod harvest index (%)

Comment [TM8]:

Comment [TM9]: Reviewer 2

Comment [TM10]: Reviewer 2

Table 4, Phenotypic mean values (PM) and predicted genotypic effects (G) of 36 genotypes for yield, yield related components and shoot traits evaluated under combined environments at MARC and AARC in 2009 and 2010

Lines	GY		PN		SN		SW		DM		CB		PHI	
	PM	G	PM	G	PM	G	PM	G	PM	G	PM	G	PM	G
GN9	2376	443**	462	130**	1777	457**	21	1.06**	91	2.66**	3657	208**	0.75	0.05**
GN50	2325	394**	438	107**	1716	398**	21	0.99**	91	2.86**	3762	313**	0.72	0.03**
GN43	2322	391**	449	118**	1705	386**	21	1.23**	91	2.82**	3568	121**	0.74	0.04**
GNL78	2306	373**	447	116**	1699	383**	21	0.73**	92	3.68**	3176	-265**	0.72	0.03**
GNL11	2271	342**	388	60**	1501	193**	21	1.04**	92	3.72**	3175	-265**	0.7	0.01*
GNL6	2254	326**	437	107**	1757	433**	21	1.21**	91	2.62**	3999	545**	0.73	0.04**
GNL60	2254	327**	436	105**	1694	377**	21	0.58**	92	3.17**	3736	287**	0.73	0.03**
GNL22	2244	318**	429	99**	1692	374**	21	1.11**	92	3.28**	3837	386**	0.74	0.04**
GNL76	2222	296**	400	70**	1556	244**	20	0.26**	91	2.75**	3033	-405**	0.69	0.01
GNL112	2206	281**	428	98**	1558	245**	21	0.73**	91	2.78**	3523	77**	0.71	0.02**
GNL7	2014	96**	364	37*	1467	159**	19	-0.38*	90	1.47*	3833	383*	0.7	0.01
GNL128	1994	86	333	6	1325	22	20	0.45**	88	-0.17	3193	-249**	0.68	-0.01
GNL67	1984	68	342	16*	1300	0.33	20	0.3	91	2.11**	3976	525**	0.68	-0.01
GNL101	1958	44	303	-22	1174	-120**	21	0.63**	89	0.39**	3290	-153**	0.68	-0.01*
GNL94	1938	25	326	-0.6	1230	-72*	21	0.63**	89	0.26	3604	156**	0.72	0.03**
GNL35	1889	-21	287	-37**	1249	-51*	19	-0.58**	88	-2.23	3115	-325**	0.68	-0.01
GNL10	1886	-25*	304	-22**	1205	-92**	20	-0.05	89	0.46**	3201	-240**	0.68	-0.01
GNL18	1873	-35	302	-24	1246	-52*	19	-0.52**	88	-0.09	3219	-221**	0.68	-0.01
GNL124	1852	-58	342	15	1337	35	20	-0.15*	88	-0.53*	3366	-77*	0.71	0.02**
GNL72	1801	-104**	269	-55**	1099	-193**	20	-0.09	87	-1.12**	3165	-275**	0.67	-0.02**
Awash-1	1789	-116**	263	-60**	1064	-228**	19	-0.44**	88	-0.39**	3130	-311**	0.66	-0.03**
GNL48	1785	-119**	280	-45**	1142	-151**	19	-0.73**	88	-0.43	3359	-85**	0.68	-0.01
GNL14	1777	-133**	276	-48**	1208	-89**	19	-0.57**	85	-2.98**	3911	456**	0.66	-0.03**
GNL27	1764	-140**	298	-27*	1232	-66**	19	-1.17**	87	-1.24**	3246	-195**	0.68	-0.01
GNL114	1748	-157**	311	-15	1216	-82*	19	-0.4**	86	-2.17**	3358	-85**	0.68	-0.01
GNL85	1706	-196**	264	-60**	1009	-280**	19	-0.39**	87	-1.12**	3320	-125**	0.66	-0.03**
GNL56	1699	-202**	274	-50**	1113	-181**	19	-0.7**	87	-1.55**	3672	223**	0.68	-0.01
GNL1	1696	-205**	259	-65**	1109	-185**	20	-0.1	87	-1.12**	3387	-61	0.69	0.01
GNL5	1693	-208**	265	-58**	1176	-120**	20	-0.08	87	-0.81*	4157	700**	0.67	-0.02
GNL90	1636	-262**	277	-48**	1096	-197**	19	-0.72**	87	-1.43**	3480	35	0.69	0.01
GNL106	1628	-271**	261	-63**	1086	-205**	19	-0.57**	85	-3.44**	4101	645**	0.67	-0.02**
GNL79	1628	-270**	257	-67**	1058	-233**	19	-0.56**	85	-3.24**	3401	-44	0.68	-0.01
GNL47	1614	-283**	255	-68**	1045	-246**	19	-1.04**	85	-3.36**	2692	-741**	0.68	-0.01
GNL93	1577	-319**	252	-72**	1024	-265**	19	-0.82**	86	-2.1**	3296	-145**	0.68	-0.01
GNL3	1562	-334**	234	-89**	1019	-271**	20	-0.27**	84	-3.58**	3294	-149**	0.66	-0.03**
GNL52	1544	-350**	234	-88**	963	-324**	19	-0.62**	84	-4.13**	2789	-644**	0.66	-0.03**

Mean	1992	326	326	1301	20	88	3445
LSD (0.05)	519		80	323	1.3	5	217

***, ** indicates** significant at 0.05 and 0.01 probability level, respectively, *LSD* least significant difference, *GY* grain yield (kg/ha), *PN* pod number per area (PN: pods m^{-2}), *SN* seed number per area (SN: seeds m^{-2}), *SW* 100 seed weight (g), *DM* days to maturity, *CB* canopy biomass (kg/ha), *PHI* pod harvest index (%)

Comment [TM11]: Reviewer 2

Comment [TM12]:

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Comment [TM14]: Reviewer 2

Table 5. Estimated variance components expressed as proportions to the phenotypic variances for all traits under drought environments

	GY	PN	SN	SW	DM	CB	PHI
V_G/Vp	0.54**	0.49**	0.46**	0.09**	0.43**	0.75**	0.57**
V_E/Vp	0.12*	0.08**	0.08**	0.22**	0.13**	0.12**	0.4**
V_{GE}/Vp	0.05**	0.03	0.06**	0.17**	0.05*	0.02	0.09**
V_{EB}/Vp	0.15**	0.12**	0.16**	0.2	0.12**	0.02*	0.1
Ve/Vp	0.25**	0.29**	0.24**	0.52**	0.27**	0.23**	0.33**

GY grain yield (kg/ha), *PN* pod number per area (PN: pods m^{-2}), *SN* seed number per area (SN: seeds m^{-2}), *SW* 100 seed weight (g), *DM* days to maturity, *CB* canopy biomass (kg/ha), *PHI* pod harvest index (%)

*, ** significant at 0.05 and 0.01 probability level, respectively. Phenotypic variance was partitioned into variances components for environmental effects (V_E), genotypic effects (V_G), environment by genotype (V_{GE}), block effects (V_B) and random error (*Ve*)

Table 6. Estimated variance components expressed as proportions to the phenotypic variances for all traits under irrigated conditions

	GY	PN	SN	SW	DM	CB	PHI
Vg/Vp	0.7**	0.6**	0.6**	0.46**	0.55**	0.82**	0.27**
V_E/Vp	0.01	0.02**	0.03**	0.03**	0.05**	0.02**	0.02*
V_{GE}/Vp	0.05**	0.11**	0.07**	0.21**	0.12**	0.02*	0.2**
V_{EB}/Vp	0.02	0.02	0.01	0.01	0.02	0.01	0.03*
Ve/Vp	0.25**	0.27**	0.3**	0.3**	0.28**	0.14**	0.48**

GY grain yield (kg/ha), *PN* pod number per area (PN: pods m^{-2}), *SN* seed number per area (SN: seeds m^{-2}), *SW* 100 seed weight (g), *DM* days to maturity, *CB* canopy biomass (kg/ha), *PHI* pod harvest index (%)

*, ** significant at 0.05 and 0.01 probability level, respectively. Phenotypic variance was partitioned into variances components for environmental effects (V_E), genotypic effects (V_G), environment by genotype (V_{GE}), block effects (V_B) and random error (*Ve*)

Table 7. Estimated variance components expressed as proportions to the phenotypic variances for all traits under all environments

	GY	PN	SN	SW	DM	CB	PHI
V_G/Vp	0.08**	0.21**	0.17**	0.09**	0.06**	0.48**	0.34**
V_E/VP	0.82**	0.51**	0.61**	0.54**	0.81**	0.3**	0.06**
V_{GE}/Vp	0.05**	0.09**	0.08**	0.14**	0.06**	0.07**	0.23**
V_{EB}/Vp	0.01**	0.04**	0.04**	0.01	0.01**	0.01*	0.01
Ve/Vp	0.04**	0.15**	0.11**	0.22**	0.06**	0.14**	0.36**

GY grain yield (kg/ha), *PN* pod number per area (PN: pods m^{-2}), *SN* seed number per area (SN: seeds m^{-2}), *SW* 100 seed weight (g), *DM* days to maturity, *CB* canopy biomass (kg/ha), *PHI* pod harvest index (%)

*, ** significant at 0.05 and 0.01 probability level, respectively. Phenotypic variance was partitioned into variances components for environmental effects (V_E), genotypic effects (V_G), environment by genotype (V_{GE}), block effects (V_B) and random error (Ve)

Table 8. Genotypic correlation analysis under drought (a) and irrigated (b) environments

(a)

	GY	PN	SN	SW	DM	CB	PHI
GY	1.00	0.96**	0.97**	0.63**	0.96**	0.25	0.93**
PN	0.96**	1.00	0.99**	0.54**	0.87**	0.29	0.93**
SN	0.97**	0.99**	1.00	0.55**	0.89**	0.30	0.93**
SW	0.63**	0.54**	0.55**	1.00	0.57**	0.24	0.63**
DM	0.96**	0.87**	0.89**	0.57**	1.00	0.24	0.86**
CB	0.25	0.29	0.30	0.24	0.24	1.00	0.26
PHI	0.93**	0.93**	0.93**	0.63**	0.86**	0.26	1.00

(b)

GY	1.00	0.97**	0.94**	0.94**	0.94**	0.21	0.81**
PN	0.97**	1.00	0.96**	0.93**	0.92**	0.29	0.84**
SN	0.94**	0.96**	1.00	0.88**	0.87**	0.37**	0.80**
SW	0.94**	0.93**	0.88**	1.00	0.90**	0.26	0.83**
DM	0.94**	0.92**	0.87**	0.90**	1.00	0.17	0.74**
CB	0.21	0.29	0.37*	0.26	0.17	1.00	0.32*
PHI	0.81**	0.84**	0.80**	0.83**	0.74**	0.32*	1.00

*, ** significant at 0.01 and 0.05 probability level, respectively. *GY* grain yield (kg/ha), *PN* pod number per area (PN: pods m^{-2}), *SN* seed number per area (SN: seeds m^{-2}), *SW* 100 seed weight (g), *DM* days to maturity, *CB* canopy biomass (kg/ha), *PHI* pod harvest index (%). The Table shows genetic correlation of seven traits under drought (a) and under irrigated condition (b).

Table 9. Genotypic correlation analysis under all environments

	GY	PN	SN	SW	DM	CB	PHI
GY	1	0.97**	0.96**	0.87**	0.95**	0.24	0.84**
PN	0.97**	1	0.99**	0.84**	0.91**	0.30**	0.91**
SN	0.96**	0.99**	1	0.82**	0.89**	0.34*	0.89**
SW	0.87**	0.84**	0.82**	1	0.82**	0.31*	0.79**
DM	0.95**	0.91**	0.89**	0.82**	1	0.24	0.79**
CB	0.24	0.3	0.34*	0.31*	0.24	1	0.31
PHI	0.84**	0.91**	0.89**	0.79**	0.79**	0.31	1

*, ** significant at 0.01 and 0.05 probability level, respectively. *GY* grain yield (kg/ha), *PN* pod number per area (PN: pods m^{-2}), *SN* seed number per area (SN: seeds m^{-2}), *SW* 100 seed weight (g), *DM* days to maturity, *CB* canopy biomass (kg/ha), *PHI* pod harvest

Comment [TM15]:

Comment [TM16]:

Comment [TM17]:

Comment [TM18]:

Comment [TM19]:

Comment [TM20]: 2nd Reviewer comments

Table 10. Canning quality traits of white pea bean genotypes

Line	Cooking Time	HC	WDW(g)	PWDW (%)	Clumping	Split	Shape	Uniformity
GNL43	26.1	1.8	275.5	67.9	4.1	2.2	2.5	3.8
GNL50	28.6	1.9	271	66.2	4.1	4.2	4.1	4.2
GNL78	30	1.8	287.5	70	4.5	4.1	4	4.3
GNL60	30	2	271.5	67.9	4.5	4.1	4	4.1
GNL9	27.5	1.8	272	69.4	4.2	2.4	2.4	4
GNL6	29.5	2.1	273	66.5	4.1	4.1	3.7	3
GNL124	30	2.1	271	64.8	4.1	2.5	3.2	3.6
GNL22	33	1.8	267.5	69.6	4.1	3.5	3.5	3.6
GNL112	27.1	1.5	271	63.3	3.4	2.3	2.9	3.3
GNL11	28.8	1.6	266.5	66.3	3.8	3.4	3.1	3.4
GNL18	27.4	1.5	265	64.6	3.4	4.5	3.3	4.1
GNL27	31.6	1.9	274	66.9	4.1	4.1	3.7	4.2
GNL5	27.9	1.6	270	63.8	3.1	3.3	2.5	3.4
GNL90	31.8	1.5	277	67.4	2.6	3.1	3.1	4.1
GNL48	28.4	1.3	270	63.7	3.5	2.4	3.5	4.1
GNL35	27	1.5	264.5	64.9	3.4	3.1	4.1	3.4
GNL94	27	1.8	269.5	69.8	3.7	3.7	2.2	3.6
GNL76	32	1.6	267.5	69	4.1	3.5	3.1	3.6
GNL1	30.3	1.7	266	66.9	3.7	3.1	2.6	3.4
GNL85	31.4	1.6	266	58.7	3.4	3.7	3.2	4.3
GNL67	26.4	2	267	63	3.7	4.1	3.4	4.4
GNL7	33.9	2	273	64.8	4.2	4	3.7	4.1
GNL93	31.2	1.8	271	62.9	3.8	3.4	3.3	3.4
Awash-1	31.1	1.8	279	66.9	4.1	3.7	3.8	3.6
Mean	29.5	1.8	271	66	3.8	3.4	3.3	3.8
LSD($_{0.05}$)	3.6	0.3	6.8	3.5	0.3	0.3	0.3	0.3

HC = hydration coefficient; WDW= washed drained weight (WDW), PWDW= Percentage Washed Drained Weight

.LSD = least significant difference

Comment [TM21]:

Comment [TM22]:

Comment [TM23]:

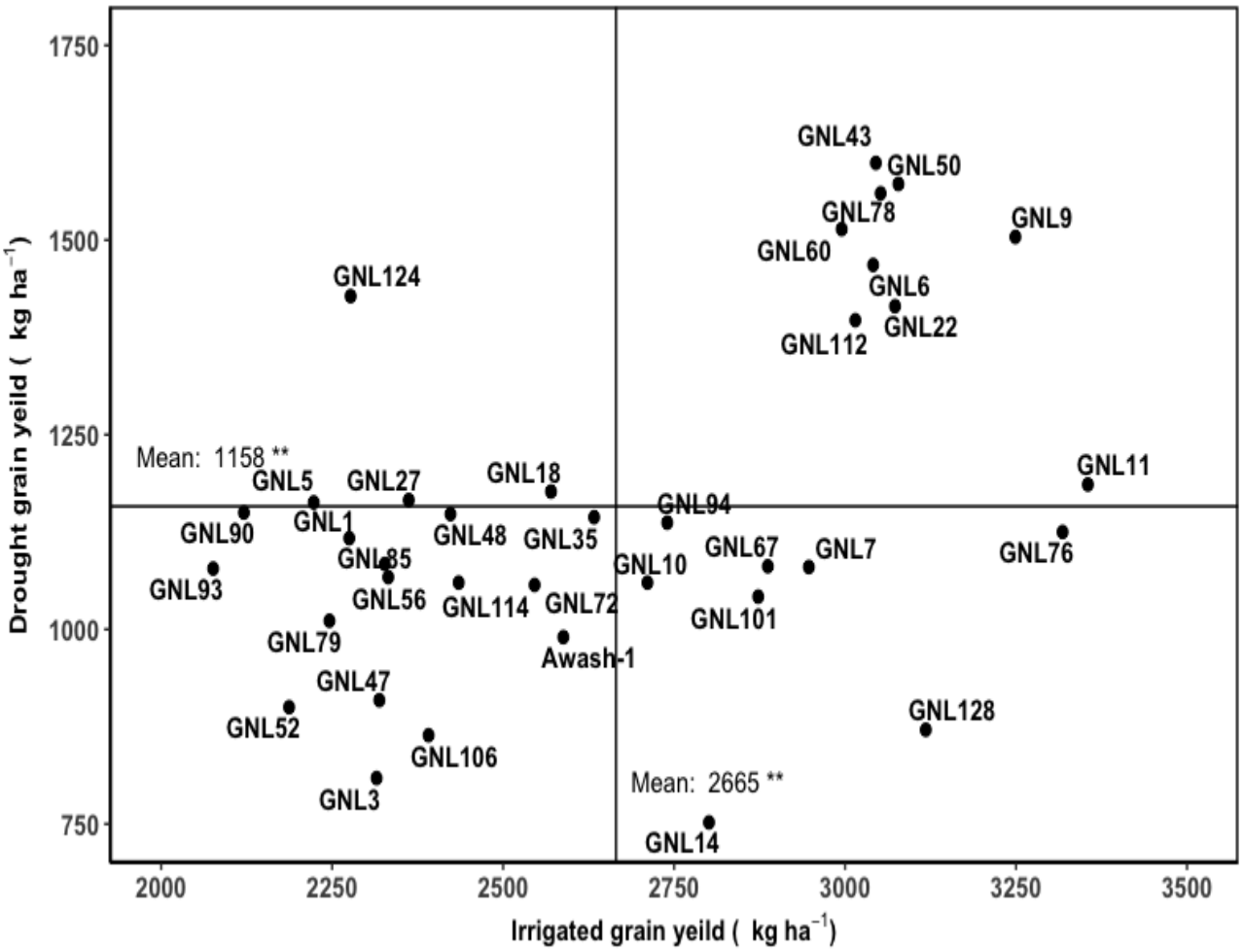

Fig. 1: Average grain yield (kg/ha) of genotypes under drought and irrigated conditions at Melkassa and Awassa, Ethiopia. Mean values for two years (2009, 2010) and two locations were used. Better yielding genotypes both under drought and irrigated conditions indicated in upper, right hand quadrant.

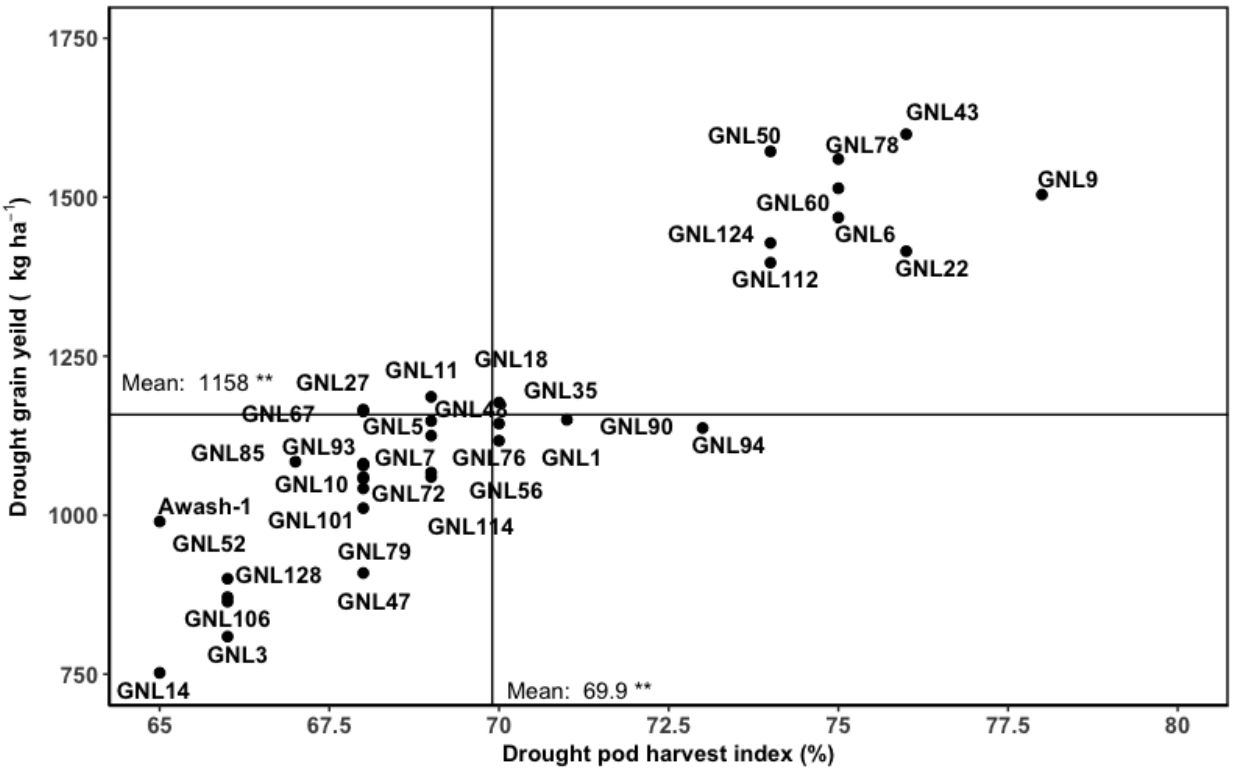

Fig. 2: Relation between grain yield (kg/ha) and pod harvest index (PHI) under drought stress at Melkassa and Awassa, Ethiopia. Mean values for two years (2009, 2010) and two locations were used. Genotypes with better grain yield and pod harvest index (PHI) indicated in the upper, right hand quadrant